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 NEWS 13  Jul 22  USAN to be reloaded July 28, 2002;
                  saved answer sets no longer valid
 NEWS 14  Jul 29  Enhanced polymer searching in REGISTRY
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                  now available on STN
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 NEWS 21  Aug 19  The MEDLINE file segment of TDXCENTER has been reloaded
 NEWS 22  Aug 26  Sequence searching in REGISTRY enhanced
 NEWS 23  Sep 03  JAPID has been reloaded and enhanced
 NEWS 24  Sep 16  Experimental properties added to the REGISTRY file
 NEWS 25  Sep 16  Indexing added to some pre-1967 records in CA/CAPLUS
 NEWS 26  Sep 16  CA Section Thesaurus available in CAPLUS and CA
 NEWS 27  Oct 01  CASREACT Enriched with Reactions from 1907 to 1985

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSIDN IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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check your SOI profiles to see if they need to be revised. For
information on CAS roles, enter HELP ROLES at an arrow prompt or use
the CAS Roles thesaurus (/RL field) in this file.

=> s review/dt
L1      1579360 REVIEW/OT

=> s anaerobic respiration
          64499 ANAEROBIC
             22 ANAEROBICS
          64506 ANAEROBIC
                  (ANAEROBIC OR ANAEROBICS)
          84444 RESPIRATION
            237 RESPIRATIONS
          84543 RESPIRATION
                  (RESPIRATION OR RESPIRATIONS)
L2          609 ANAEROBIC RESPIRATION
                  (ANAEROBIC(W)RESPIRATION)

=> oxidant source
OXIOANT IS NOT A RECOGNIZED COMMANO
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANOS" at an arrow prompt (=>).

=> s oxidant source
          32262 OXIOANT
          12889 OXIOANTS
          40646 OXIDANT
                  (OXIDANT OR OXIDANTS)
         482197 SOURCE
         241181 SOURCES
         646429 SOURCE
                  (SOURCE OR SOURCES)
L3           34 OXIOANT SOURCE
                  (OXIOANT(W)SOURCE)

=> s l1 and l2
L4           61 L1 ANO L2

=> l3 and l4
L3 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANOS" at an arrow prompt (=>).

=> s l3 and l4
L5            0 L3 AND L4

=> s bacteria
         238584 BACTERIA
             73 BACTERIAS
L6       238628 BACTERIA
                  (BACTERIA OR BACTERIAS)
```

=> s l4 and l6
L7 27 L4 AND L6

=> d ab bib l7 tot

L7 ANSWER 1 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review. The orbital structure of mol. oxygen constrains it to accept electrons one at a time, and its unfavorable univalent redn. potential ensures that it can do so only with low-potential redox partners. In E. coli, this restriction prevents oxygen from oxidizing structural mols. Instead, it primarily oxidizes reduced flavins, a reaction that is harmful only in that it generates superoxide and hydrogen peroxide as products. These species are stronger oxidants than is oxygen itself. They can oxidize dehydratase iron-sulfur clusters and sulphydryls, resp., and thereby inactivate enzymes that are dependent upon these functional groups. Hydrogen peroxide also oxidizes free iron, generating hydroxyl radicals. Because hydroxyl radicals react with virtually any biomols. they encounter, their reactivity is broadly dissipated, and only their reactions with DNA are known to have an important physiol. impact. E. coli elaborates scavenging and repair systems to minimize the impact of this adventitious chem.; mutants that lack these defences grow poorly in aerobic habitats. Some of the growth deficits of these mutants cannot be easily ascribed to sulphydryl, cluster, or DNA damage, indicating that important aspects of oxidative stress still lack a biochem. explanation. Obligate anaerobes cannot tolerate oxygen because they utilize metabolic schemes built around enzymes that react with oxidants. The reliance upon low-potential flavoproteins for ***anaerobic*** ***respiration*** probably causes substantial superoxide and hydrogen peroxide to be produced when anaerobes are exposed to air. These species then generate damage of the same type that they produce in aerotolerant ***bacteria*** . However, obligate anaerobes also utilize several classes of dioxygen-sensitive enzymes that are not needed by aerobes. These enzymes are used for processes that help maintain the redox balance during anaerobic fermns. They catalyze reactions that are chem. difficult, and the reaction mechanisms require the solvent exposure of radicals or low-potential metal clusters that can react rapidly with oxygen. Recent work has uncovered adaptive strategies by which obligate anaerobes seek to minimize the damage done by superoxide and hydrogen peroxide. Their failure to divest themselves of enzymes that can be directly damaged by mol. oxygen suggests that evolution has not yet provided economical options to them. (c) 2002 Academic Press.
AN 2002:546507 CAPLUS
DN 137:137306
TI How oxygen damages microbes: Oxygen tolerance and obligate anaerobiosis
AU Imlay, James A.
CS Department of Microbiology, University of Illinois, Urbana, IL, 61801, USA
SO Advances in Microbial Physiology (2002), 46, 111-153
CODEN: AMIPB2; ISSN: 0065-2911
PB Academic Press
DT Journal; ***General Review***
LA English
RE.CNT 163 THERE ARE 163 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review. The dimethylsulfoxide (DMSO) reductase family of molybdenum enzymes is a large and diverse group that is found in ***bacteria*** and archaea. These enzymes are characterized by a bis(molybdopterin guanine dinucleotide)Mo form of the molybdenum cofactor, and they are particularly important in ***anaerobic*** ***respiration*** including the dissimilatory redn. of certain toxic oxoanions. The structural and phylogenetic relationship between the proteins of this family is discussed. High-resoln. crystal structures of enzymes of the DMSO reductase family have revealed a high degree of similarity in tertiary structure. However, there is considerable variation in the structure of the molybdenum active site and it seems likely that these subtle but important differences lead to the great diversity of function seen in this family of enzymes. This diversity of catalytic capability is assocd. with several distinct pathways of electron transport.
AN 2002:221366 CAPLUS
DN 136:397653
TI The DMSO reductase family of microbial molybdenum enzymes; molecular properties and role in the dissimilatory reduction of toxic elements
AU McEwan, Alastair G.; Ridge, Justin P.; McDevitt, Christopher A.; Hugenholtz, Philip
CS Centre for Metals in Biology Department of Microbiology and Parasitology School of Molecular and Microbial Sciences, University of Queensland, St.

Luçia, Australia
SO Geomicrobiology Journal (2002), 19(1), 3-21
CODEN: GEJODG; ISSN: 0149-0451
PB Taylor & Francis Ltd.
DT Journal; ***General Review***
LA English
RE.CNT 76 THERE ARE 76 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 54 refs. Although closely related phylogenetically and sharing many phenotypic similarities, Campylobacter jejuni and Helicobacter pylori are distinct in some major aspects of their physiol. and metab. In this paper, comparative aspects of the physiol. of these pathogens is discussed in the light of recent biochem. and genome sequence data. Campylobacter jejuni is emerging as a more versatile and metabolically active pathogen, with a complete citric acid cycle, and a complex and highly branched respiratory chain which allows both aerobic and ***anaerobic*** ***respiration*** with a variety of alternative electron acceptors. These properties enable it to survive in a no. of environments in addn. to the mammalian or avian gut. In vivo, anaerobic growth of C. jejuni could be an important factor allowing intestinal colonization. Helicobacter pylori is a more specialized pathogen, largely restricted to the human stomach, with a unique combination of virulence factors, an incomplete citric acid cycle, a simpler respiratory chain with only a single terminal oxidase and fewer regulatory systems. Both ***bacteria*** are microaerophiles and, while there is likely to be no single explanation for their oxygen sensitivity, there is evidence that the possession of oxygen-sensitive enzymes and an increased sensitivity to oxidative stress play an important role.
AN 2001:562849 CAPLUS
DN 135:269748
TI The physiology and metabolism of Campylobacter jejuni and Helicobacter pylori
AU Kelly, D. J.
CS Department of Molecular Biology and Biotechnology, University of Sheffield, Sheffield, S10 2TN, UK
SO Society for Applied Microbiology Symposium Series (2001), 30(Campylobacter, Helicobacter and Arcobacter), 16S-24S
CODEN: SMSSFP; ISSN: 0267-4440
PB Blackwell Science Ltd.
DT Journal; ***General Review***
LA English
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 44 refs. Ecol. studies have shown that water-contg. terrestrial, subterranean and submarine high-temp. environments harbor a great diversity of hyperthermophilic prokaryotes, growing fastest at temps. of 80.degree.C or above. The investigations included cultivation, isolation and detailed anal. of these hyperthermophiles as well as in situ 16S rRNA gene sequence anal. and in situ hybridization studies. For a safe and fast isolation of novel hyperthermophiles from mixed cultures, a new, plating-independent isolation technique was developed, based on the use of a laser microscope (optical tweezers). This method, combined with 16S rRNA gene sequence anal. and whole-cell hybridization using fluorescently labeled oligonucleotide probes, even allows the recovery of pure cultures of phylogenetically predicted organisms harboring novel 16S rRNA gene sequences. In their natural habitats, hyperthermophiles form complex food webs, consisting of primary producers and consumers of org. material. Their metabolic potential includes various types of aerobic and ***anaerobic*** ***respiration*** and different modes of fermn. In hydrothermal and geothermal environments, hyperthermophiles have important ecol. functions in biogeochem. processes. Members of the Sulfolobales are able to mobilize heavy metals from sulfidic ores like pyrite or chalcopyrite. Biomineralization processes of hyperthermophiles include the formation of magnetite from iron or the pptn. of arsenate as realgar, a reaction performed by a novel hyperthermophile that was isolated from Pisciarelli Solfatara, Naples, Italy.
AN 2000:804727 CAPLUS
DN 134:83154
TI Towards the ecology of hyperthermophiles: biotopes, new isolation strategies and novel metabolic properties
AU Huber, R.; Huber, H.; Stetter, K. O.
CS Lehrstuhl fur Mikrobiologie und Archaeenzentrum, Universitat Regensburg,

Regensburg, D-93053, Germany
SO FEMS Microbiology Reviews (2000), 24(5), 615-623
CODEN: FMREE4; ISSN: 0168-6445
PB Elsevier Science B.V.
DT Journal; ***General Review***
LA English
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 45 refs. The genus Propionibacterium includes dairy and cutaneous propionibacteria; they differ principally by their natural habitats: in milks, cheeses and on human skin and in the rumen ruminants resp. Using modern methods of mol. biol. a new compn. of the genus, contg. at present 10 species was established. These ***bacteria*** generate energy by fermn., which is linked with a short ***anaerobic*** ***respiration*** chain yielding more ATP than in any other bacterial fermn. Propionibacteria contain the app. for the aerobic lifestyle including antioxidative defense systems consisting of SOD, catalase and peroxidase. The metab. of anaerobic species of propionic acid ***bacteria*** (PAB) is tuned to the use of a high level of vitamin B12, which participates not only in fermn., but in a no. of vital anabolic reactions too. In the absence of vitamin B12 PAB switch to a B12-independent way of existence, which is, however, less effective than the B12-dependent one. Cells, culture liqs. (CL) and cell exts. possess antimutagenic (AM) activity. AM activity of CL is linked with an extracellular protein(s). The proteinaceous cytosolic fraction of propionibacteria exerts reactivative activity on pro- and eukaryotic organisms subjected to different and unrelated stresses. The physiol. peculiarities of PAB open up new areas of their practical applications: the possibility of creation of medical and prophylactic prepns. with AM and antistress properties, prepns. with antioxidative properties, SOD and of human probiotics that may be useful in the biotechnol. of environmental health.
AN 2000:726320 CAPLUS
DN 134:68463
TI Physiological peculiarities of propionibacteria - present facts and prospective applications
AU Vorobjeva, Lena
CS Biology Faculty, Moscow State University, Moscow, 119899, Russia
SO Science Progress (Northwood, United Kingdom) (2000), 83(3), 277-301
CODEN: SCPRAY; ISSN: 0036-8504
PB Science Reviews Ltd.
DT Journal; ***General Review***
LA English
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 6 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with many refs. ***Bacteria*** are the most remarkable organisms in the biosphere, surviving and growing in environments that support no other life forms. Underlying this ability is a flexible metab. controlled by a multitude of environmental sensors and regulators of gene expression. It is not surprising, therefore, that bacterial respiration is complex and highly adaptable: virtually all ***bacteria*** have multiple, branched pathways for electron transfer from numerous low-potential reductants to several terminal electron acceptors. Such pathways, particularly those involved in ***anaerobic*** ***respiration*** , may involve periplasmic components, but the respiratory app. is largely membrane-bound and organized such that electron flow is coupled to proton (or sodium ion) transport, generating a protonmotive force. It has long been supposed that the multiplicity of pathways serves to provide flexibility in the face of environmental stresses, but the existence of apparently redundant pathways for electrons to a single acceptor, say dioxygen, is harder to explain. Clues have come from studying the expression of oxidases in response to growth conditions, the phenotypes of mutants lacking one or more oxidases, and biochem. characterization of individual oxidases. Terminal oxidases that share the essential properties of substrate (cytochrome c or quinol) oxidn., dioxygen redn. and, in some cases, proton translocation, differ in subunit architecture and complement of redox centers. Perhaps more significantly, they differ in their affinities for oxidant and reductant, mode of regulation, and inhibitor sensitivity; these differences to some extent rationalize the presence of multiple oxidases. However, intriguing requirements for particular functions in certain physiol. functions remain unexplained. For example, a large body of evidence demonstrates that cytochrome bd is essential for growth and survival under certain

conditions. In this review, the physiol. basis of the many phenotypes of Cyd- mutants is explored, particularly the requirement for this oxidase in diazotrophy, growth at low protonmotive force, survival in the stationary phase, and resistance to oxidative stress and Fe(III) chelators. (c) 2000 Academic Press.

AN 2000:568364 CAPLUS
DN 133:263575
TI Redundancy of aerobic respiratory chains in ***bacteria*** ? Routes, reasons and regulation
AU Poole, Robert K.; Cook, Gregory M.
CS Krebs Institute for Biomolecular Research, University of Sheffield, Sheffield, S10 2TN, UK
SO Advances in Microbial Physiology (2000), 43, 165-224
CODEN: AMIPB2; ISSN: 0065-2911
PB Academic Press
DT Journal; ***General Review***
LA English
RE.CNT 225 THERE ARE 225 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 121 refs. Facultative ***bacteria*** have developed a variety of regulatory mechanisms to adapt to changes in the availability of oxygen. Several global regulatory proteins and their cofactors have been identified, and despite the metabolic diversity among different organisms, common features of oxygen-sensing proteins are emerging. Thus far, a heme group, a flavin moiety, and an Fe-S cluster have been assigned a function as cofactors in oxygen-sensing proteins. Oxygen concns. seem to be sensed both directly and indirectly. Some regulators are distinguished by a conserved PAS domain whose specificity in signal sensing seems to vary according to the assocd. cofactor. This review summarizes the current knowledge about the oxygen-dependent expression of three well-studied metabolic pathways: ***anaerobic*** ***respiration*** in Escherichia coli, anoxygenic photosynthesis in purple nonsulfur ***bacteria*** , and nitrogen fixation in both the free-living and symbiotic N2-fixing ***bacteria*** . It will show that oxygen-dependent regulation of these pathways often consists of sophisticated overlapping regulatory circuits involving different types of oxygen sensory proteins resulting in stringent control of gene expression in response to oxygen availability.

AN 2000:545455 CAPLUS
DN 133:249349
TI Mechanisms for sensing and responding to oxygen deprivation
AU Patschkowski, Thomas; Bates, Donna M.; Kiley, Patricia J.
CS Department of Biomolecular Chemistry, University of Wisconsin Medical School, Madison, WI, 53706, USA
SO Bacterial Stress Responses (2000), 61-78. Editor(s): Storz, Gisela; Hengge-Aronis, Regine. Publisher: ASM Press, Washington, D. C.
CODEN: 69AFY8
DT Conference; ***General Review***
LA English
RE.CNT 134 THERE ARE 134 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 160 refs. Helicobacter pylori is a gram-neg. ***bacteria*** which colonizes the gastric mucosa of humans and is implicated in a wide range of gastroduodenal diseases. This paper reviews the physiol. of this bacterium as predicted from the sequenced genomes of two unrelated strains and reconciles these predictions with the literature. In general, the predicted capabilities are in good agreement with reported exptl. observations. H. pylori is limited in carbohydrate utilization and will use amino acids, for which it has transporter systems, as sources of carbon. Energy can be generated by fermn., and the bacterium possesses components necessary for both aerobic and ***anaerobic*** ***respiration*** . Sulfur metab. is limited, whereas nitrogen metab. is extensive. There is active uptake of DNA via transformation and ample restriction-modification activities. The cell contains numerous outer membrane proteins, some of which are porins or involved in iron uptake. Some of these outer membrane proteins and the lipopolysaccharide may be regulated by a slipped-strand repair mechanism which probably results in phase variation and plays a role in colonization. In contrast to a commonly held belief that H. pylori is a very diverse species, few differences were predicted in the physiol. of these two unrelated strains, indicating that host and environmental factors probably play a significant role in the outcome of H. pylori-related disease.

AN 1999:624326 CAPLUS
DN 132:10543
TI Helicobacter pylori physiology predicted from genomic comparison of two strains
AU Doig, Peter; De Jonge, Boudewijn L.; Alm, Richard A.; Brown, Eric D.; Uria-Nickelsen, Maria; Noonan, Brian; Mills, Scott D.; Tummino, Peter; Carmel, Gilles; Guild, Braydon C.; Moir, Donald T.; Vovis, Gerald F.; Trust, Trevor J.
CS AstraZeneca R&D Boston, Cambridge, MA, 02139, USA
SO Microbiology and Molecular Biology Reviews (1999), 63(3), 675-707
CODEN: MMBRF7; ISSN: 1092-2172
PB American Society for Microbiology
DT Journal; ***General Review***
LA English
RE.CNT 160 THERE ARE 160 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 308 refs. The publication of the complete sequence of Helicobacter pylori 26695 in 1997 and more recently that of strain J99 has provided new insight into the biol. of this organism. In this review, we attempt to analyze and interpret the information provided by sequence annotations and to compare these data with those provided by exptl. analyses. After a brief description of the general features of the genomes of the two sequenced strains, the principal metabolic pathways are analyzed. In particular, the enzymes encoded by H. pylori involved in fermentative and oxidative metab., lipopolysaccharide biosynthesis, nucleotide biosynthesis, aerobic and ***anaerobic*** ***respiration*** , and iron and nitrogen assimilation are described, and the areas of controversy between the exptl. data and those provided by the sequence annotation are discussed. The role of urease, particularly in pH homeostasis, and other specialized mechanisms developed by the bacterium to maintain its internal pH are also considered. The replicational, transcriptional, and translational apparatuses are reviewed, as is the regulatory network. The numerous findings on the metab. of the ***bacteria*** and the paucity of gene expression regulation systems are indicative of the high level of adaptation to the human gastric environment. Arguments in favor of the diversity of H. pylori and mol. data reflecting possible mechanisms involved in this diversity are presented. Finally, the authors compare the numerous exptl. data on the colonization factors and those provided from the genome sequence annotation, in particular for genes involved in motility and adherence of the bacterium to the gastric tissue.
AN 1999:624325 CAPLUS
DN 131:348825
TI Metabolism and genetics of Helicobacter pylori: the genome era
AU Marais, Armelle; Mendz, George L.; Hazell, Stuart L.; Megraud, Francis
CS Laboratoire de Bacteriologie, Universite Victor Segalen, Bordeaux, 33076, Fr.
SO Microbiology and Molecular Biology Reviews (1999), 63(3), 642-674
CODEN: MMBRF7; ISSN: 1092-2172
PB American Society for Microbiology
DT Journal; ***General Review***
LA English
RE.CNT 308 THERE ARE 308 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 172 refs. Helicobacter pylori is a spiral Gram-neg. microaerophilic bacterium that causes one of the most common infections in humans; approx. 30-50% of individuals in Western Europe are infected and the figure is nearly 100% in the developing world. It is recognized as the major etiol. factor in chronic active type B gastritis, and gastric and duodenal ulceration and as a risk factor for gastric cancer. H. pylori normally inhabits the mucus-lined surface of the antrum of the human stomach where it induces a mild inflammation, but its presence is otherwise usually asymptomatic. A variety of virulence factors appear to play a role in pathogenesis. These include the vacuolating cytotoxin VacA, cytotoxin-assocd. proteins, urease and motility. All are under intense study in an attempt to understand how the bacterium colonizes and persists in the gastric mucosa, and how H. pylori infections lead to the disease state. Although an explosion of research on H. pylori has occurred within the past 15 yr, most efforts have been directed at aspects of the bacterium and disease process which are of direct clin. relevance. Consequently, our knowledge of many aspects of the physiol. and metab. of H. pylori is relatively poor. This should change rapidly now that the complete genome sequence of a pathogenic strain has been detd. This

review focuses attention on these more fundamental areas of Helicobacter biol. Anal. of the genome sequence and some detailed metabolic studies have revealed solute transport systems, an incomplete citric acid cycle and several incomplete biosynthetic pathways, which largely explain the complex nutritional requirements of H. pylori. The microaerophilic nature of the bacterium is of particular interest and may be due in part to the involvement of oxygen-sensitive enzymes in central metabolic pathways. However, the biochem. basis for the requirement for CO_2 has not been completely explained and a major surprise is the apparent lack of anaplerotic carboxylation enzymes. Although genes for glycolytic enzymes are present, physiol. studies indicate that the Entner-Doudoroff and pentose phosphate pathways are more active. The respiratory chain is remarkably simple, apparently with a single terminal oxidase and fumarate reductase as the only reductase for ***anaerobic*** ***respiration*** . NADPH appears to be the preferred electron donor in vivo, rather than NADH as in most other ***bacteria*** . H. pylori is not an acidophile, and must possess mechanisms to survive stomach acid. Many studies have been carried out on the role of the urease in acid tolerance but mechanisms to maintain the protonmotive force at low external pH values may also be important, although poorly understood at present. In terms of the regulation of gene expression, there are few regulatory and DNA binding proteins in H. pylori, esp. the two-component sensor-regulator systems, which indicates a minimal degree of environmentally responsive gene expression. (c) 1998 Academic Press.

AN 1999:6428 CAPLUS
DN 130:194003
TI The physiology and metabolism of the human gastric pathogen Helicobacter pylori
AU Kelly, David J.
CS Department of Molecular Biology and Biotechnology, University of Sheffield, Sheffield, S10 2TN, UK
SO Advances in Microbial Physiology (1998), 40, 137-189
CODEN: AMIPB2; ISSN: 0065-2911
PB Academic Press
DT Journal; ***General Review***
LA English
RE.CNT 172 THERE ARE 172 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 27 CAPLUS COPYRIGHT 2002 ACS

AB A review with 30 refs. The facultatively anaerobic Escherichia coli is able to grow by aerobic and by ***anaerobic*** ***respiration*** . Despite the large difference in the amt. of free energy that could maximally be conserved from aerobic vs. ***anaerobic*** ***respiration*** , the proton potential and .DELTA.G'Phos are similar under both conditions. O_2 represses ***anaerobic*** ***respiration*** , and nitrate represses fumarate respiration. By this the terminal reductases of aerobic and ***anaerobic*** ***respiration*** are expressed in a way to obtain maximal H+/e- ratios and ATP yields. The respiratory dehydrogenases, on the other hand, are not synthesized in a way to achieve maximal H+/e- ratios. Most of the dehydrogenases of aerobic respiration do not conserve redox energy in a proton gradient whereas the enzymes from ***anaerobic*** ***respiration*** do so. Thus transcriptional regulation of the respiratory pathways by electron acceptors has multiple effects on cellular energetics. The transcriptional regulation in response to O_2 is effected by two transcriptional regulators, ArcA/B (aerobic respiratory control) and FNR (fumarate nitrate reductase regulator). FNR contains an O_2-sensitive [4Fe-4S]2+ cluster in the sensory domain and is converted to the transcriptional inactive state in the presence of (cytoplasmic) O_2.

AN 1998:456083 CAPLUS
DN 129:158891
TI Transcriptional regulation and energetics of alternative respiratory pathways in facultatively anaerobic ***bacteria***
AU Unden, Gottfried
CS Institut fur Mikrobiologie und Weinforschung, Univ. Mainz, Mainz, 55099, Germany
SO Biochimica et Biophysica Acta (1998), 1365(1-2), 220-224
CODEN: BBACAQ; ISSN: 0006-3002
PB Elsevier Science B.V.
DT Journal; ***General Review***
LA English

L7 ANSWER 12 OF 27 CAPLUS COPYRIGHT 2002 ACS

AB A review, with 175 refs., on deoxyadenosylcobalamin (Ado-B12) biosynthesis, transport, use, and uneven distribution among living forms. We describe how genetic anal. of enteric ***bacteria*** has

contributed to these issues. Two pathways for corrin ring formation have been found-an aerobic pathway (in P. denitrificans) and an anaerobic pathway (in P. shermanii and S. typhimurium)-that differ in the point of cobalt insertion. Anal. of B12 transport in E. coli reveals two systems: one (with two proteins) for the outer membrane, and one (with three proteins) for the inner membrane. To account for the uneven distribution of B12 in living forms, we suggest that the B12 synthetic pathway may have evolved to allow anaerobic fermn. of small mols. in the absence of an external electron acceptor. Later, evolution of the pathway produced siroheme, (allowing use of inorg. electron acceptors), chlorophyll (O2 prodn.), and heme (aerobic respiration). As oxygen became a larger part of the atm., many organisms lost fermentative functions and retain dependence on newer, B12 functions that did not involve fermn. Paradoxically, Salmonella spp. synthesize B12 only anaerobically but can use B12 (for degrdn. of ethanolamine and propanediol) only with oxygen. Genetic anal. of the operons for these degradative functions indicate that anaerobic degrdn. is important. Recent results suggest that B12 can be synthesized and used during ***anaerobic*** ***respiration*** using tetrathionate (but not nitrate or fumarate) as an electron acceptor. The branch of enteric taxa from which Salmonella spp. and E. coli evolved appears to have lost the ability to synthesize B12 and the ability to use it in propanediol and glycerol degrdn. Salmonella spp., but not E. coli, have acquired by horizontal transfer the ability to synthesize B12 and degrade propanediol. The acquired ability to degrade propanediol provides the selective force that maintains B12 synthesis in this group.

AN 1996:615231 CAPLUS
DN 125:268755
TI Cobalamin (coenzyme B12): synthesis and biological significance
AU Roth, J. R.; Lawrence, J. G.; Bobik, T. A.
CS Dep. Biol., Univ. Utah, Salt Lake City, UT, 84112, USA
SO Annual Review of Microbiology (1996), 50, 137-181
CODEN: ARMIAZ; ISSN: 0066-4227
PB Annual Reviews
DT Journal; ***General Review***
LA English

L7 ANSWER 13 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 48 refs. Considerable progress has been made towards enhancing our understanding of the phylogeny, ecol. and biogeochem. role of dissimilatory iron-reducing ***bacteria*** . The known phylogenetic range of iron-reducing ***bacteria*** has expanded considerably, as has the known range of iron minerals that serve as a source of Fe(III) for ***anaerobic*** ***respiration*** . In addn., the no. of biotechnol. applications of iron-reducing ***bacteria*** , including remediation of soils and sediments contaminated with metals, radionuclides and orgs., is rapidly expanding.
AN 1996:386490 CAPLUS
DN 125:53108
TI Environmental processes mediated by iron-reducing ***bacteria***
AU Fredrickson, James K.; Gorby, Yuri A.
CS Pacific Northwest National Laboratory, Richland, WA, 99352, USA
SO Current Opinion in Biotechnology (1996), 7(3), 287-294
CODEN: CUOBE3; ISSN: 0958-1669
PB Current Biology
DT Journal; ***General Review***
LA English

L7 ANSWER 14 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 224 refs. Aerobic and anaerobic electron transport chains of facultative phototrophs have been of increasing interest because of their diverse organization of redox carriers and their adaptive regulatory mechanisms of gene expression. During the last decade, studies on the biochem. of bacterial redox complexes such as NADH-dh and bc1 from Rhodobacter species, and cyt c-oxidases of aa3 type from R. sphaeroides and Chloroflexus aurantiacus, have revealed the presence of fewer subunits than corresponding eukaryotic enzymes. This evidence has provided new insights into the biochem. evolution of respiration and also useful indications on structure/function relationships. Recent advances in studying the aerobic and anaerobic respiratory pathways of facultative phototrophs have taken advantage of modern mol. genetics. In particular, the role of sol. cytochrome c2, until recent years considered to be essential for electron transport in the two closely related species Rb. capsulatus and Rb. sphaeroides, has been better defined. Indeed, it is now clear that two different classes of alternative electron carriers (sol. cyt iso-c2 and membrane-bound cyt cy) can operate between the membrane-bound redox complexes instead of, or along with, the cyt c2. The presence of multiple electron carriers between redox complexes suggests

that cyt cy-like components might be more widely spread among those photosynthetic ***bacteria*** where photooxidizable soluble c-type hemes are not readily detected, e.g. C. aurantiacus. The outstanding metabolic versatility of R. capsulatus made also possible the use of mutants defective in redox carriers of aerobic respiration for the anal. of anaerobic electron transport pathways. Thus, if the role of cyt c2 in anaerobic light-driven electron flow has partially been reshuffled, cyt c2 seems to play a key role in the dark anaerobic pathways leading to NO2 and N2 redn. The use of cyt c-deficient mutants also demonstrated that the ubiquinol-cyt c oxidoreductase is not required for growth with DMSO or TMAO as electron acceptors. These dark anaerobic processes, however, cannot sustain a consistent cell growth in the presence of nonfermentable substrates; thus they must be regarded as advantageous metabolic systems facilitating anaerobic growth in the dark and/or light.

AN 1996:224560 CAPLUS
DN 124:255336
TI Aerobic and anaerobic electron transport chains in anoxygenic phototrophic ***bacteria***
AU Zannoni, Davide
CS Department Biology, University Bologna, Bologna, 40126, Italy
SO Advances in Photosynthesis (1995), 2(Anoxygenic Photosynthetic Bacteria), 949-71
CODEN: ADPHFM; ISSN: 1382-4252
PB Kluwer
DT Journal; ***General Review***
LA English

L7 ANSWER 15 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 101 refs. Purple nonsulfur photosynthetic ***bacteria*** are probably the most versatile of all microorganisms. Besides growing photoautotrophically or photoheterotrophically, they can also develop chemotrophically in darkness under aerobic conditions. Moreover, some of these ***bacteria*** are capable of dark ***anaerobic*** ***respiration*** . The photosynthetic and respiratory chains are localized in two different regions of the membrane, the intracytoplasmic and the cytoplasmic parts, resp. This variety in bioenergetic pathways allows the ***bacteria*** to accommodate changes in the available sources of energy and in environmental factors. A first level of regulation concerns the biosynthesis of electron transfer components. A second regulation concerns the interactions between these different processes. Here, emphasis is placed on the interactions and the organization of these different electron transport chains. The ***bacteria*** utilize preferentially the light as energy source. In darkness, the use of the electron acceptor with the highest redox potential allows the ***bacteria*** to recover the max. free energy. Two different mechanisms are responsible for these interactions. First the proton motive force, delocalized on the internal membrane, exerts a thermodn. back pressure on the first complexes of respiratory chains. Second, modulation is mediated by changes in the redox state of electron carriers involved in the different bioenergetic processes. Two distinct pools of cytochrome c2, a periplasmic electron carrier, have been found. A first pool, localized in the periplasmic space, is connected to the respiratory chains but can be photooxidized by the small no. of reaction centers present in the cytoplasmic part of the membrane. This photooxidn. inhibits the respiratory activities. The second pool is assocd. with the intracytoplasmic membrane. One cytochrome c2, two reaction centers and one cytochrome bc1 complex are organized in a supercomplex where the electron transfer is confined. This supermol. organization allows for a very efficient photoinduced cyclic electron transfer not limited by the diffusion of the reactants. The stability of the supercomplex depends upon different factors like the redox state of cytochrome c2, the pH and the presence of divalent cations. Different mechanisms for their formation are discussed.

AN 1996:224530 CAPLUS
DN 124:255687
TI Organization of electron transfer components and supercomplexes
AU Vermeglio, Andre; Joliot, Pierre; Joliot, Anne
CS DPVE/SBC CE Cadarache, CEA, Saint Paul-lez-Durance, 13108, Fr.
SO Advances in Photosynthesis (1995), 2(Anoxygenic Photosynthetic Bacteria), 279-95
CODEN: ADPHFM; ISSN: 1382-4252
PB Kluwer
DT Journal; ***General Review***
LA English

L7 ANSWER 16 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 64 refs. Many microbes use sulfonate-sulfur as the sole

sulfur source for biosynthesis even when the carbon of that sulfonate cannot be used as an energy source for growth. Studies of ***bacteria*** , including members of the genera Comamonas and Escherichia, as well as ascomycetous and basidiomycetous yeasts indicate that the sulfur of many naturally occurring sulfonates can be reduced and assimilated into cellular sulfur compds. during aerobic, respiratory growth. Other unrelated ***bacteria*** (e.g., members of the genera Clostridium, Klebsiella) are able to use sulfonate-sulfur for biosynthesis under anaerobic conditions. Sulfonate can also serve as the terminal electron acceptor for Desulfovibrio's ***anaerobic*** ***respiration*** . The breadth of microbial participation in sulfonate-sulfur transformations in the natural sulfur cycle is thus established.

AN 1995:992034 CAPLUS
DN 124:25255
TI Microbial assimilation and dissimilation of sulfonate sulfur
AU Seitz, A. P.; Leadbetter, E. R.
CS Dep. Mol. Cell Biol., Univ. Connecticut, Storrs, CT, 06269-2131, USA
SO ACS Symposium Series (1995), 612(Geochemical Transformations of Sedimentary Sulfur), 365-76
CODEN: ACSMC8; ISSN: 0097-6156
PB American Chemical Society
DT Journal; ***General Review***
LA English

L7 ANSWER 17 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with many refs. Purple non-sulfur phototrophic ***bacteria*** , exemplified by Rhodobacter capsulatus and Rhodobacter sphaeroides, exhibit a remarkable versatility in their anaerobic metab. In these ***bacteria*** the photosynthetic app., enzymes involved in CO2 fixation and pathways of ***anaerobic*** ***respiration*** are all induced upon a redn. in oxygen tension. Recently, there have been significant advances in the understanding of mol. properties of the photosynthetic app. and the control of the expression of genes involved in photosynthesis and CO2 fixation. In addn., anaerobic respiratory pathways have been characterized and their interaction with photosynthetic electron transport has been described. This review will survey these advances and will discuss the ways in which photosynthetic electron transport and oxidn.-redn. processes are integrated during photoautotrophic and photoheterotrophic growth.

AN 1995:368288 CAPLUS
DN 122:128167
TI Photosynthetic electron transport and anaerobic metabolism in purple non-sulfur phototrophic ***bacteria***
AU McEwan, Alastair G.
CS Department of Microbiology, University of Queensland, Brisbane, 4072, Australia
SO Antonie van Leeuwenhoek (1994), 66(1-3), 151-64
CODEN: ALJMAO; ISSN: 0003-6072
PB Kluwer
DT Journal; ***General Review***
LA English

L7 ANSWER 18 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 60 refs. describing FNR protein homologs in ***bacteria*** other than E. coli, focusing on the roles that these proteins play in regulating cellular physiol., and considering some of the conserved structural features in this family of regulatory proteins. Homologs of the transcriptional regulator FNR from Escherichia coli have been identified in a variety of taxonomically diverse bacterial species. Despite being structurally very similar, members of the FNR family have disparate regulatory roles. Those from Shewanella putrefaciens, Pseudomonas aeruginosa, Pseudomonas stutzeri and Rhodopseudomonas palustris are functionally similar to FNR in that they regulate ***anaerobic*** ***respiration*** or carbon metab. Four rhizobial proteins (from Rhizobium meliloti, R. leguminosarum, B. japonicum and Azorhizobium caulinodans) are involved in the regulation of nitrogen fixation; a fifth (from Rhizobium strain IC3342) has unknown function. Two proteins from mammalian pathogens (Actinobacillus pleuropneumoniae and Bordetella pertussis) may be involved in the regulation of toxin expression. The FNR protein of Vibrio fischeri regulates bioluminescence, and the function of the one known FNR homolog from a Gram-pos. organism (Lactobacillus casei) remains to be elucidated. Some members of this family, like FNR itself, appear to function as sensors of oxygen availability, whereas others do not. The ability to sense and respond to oxygen limitation may be correlated with the presence of cysteine residues which, in the case of FNR, are thought to be involved in oxygen or redox

sensing. The mechanism of DNA sequence recognition is probably conserved, or very similar, throughout this family. In a no. of other Gram-neg. species, there is good indirect evidence for the existence of FNR analogs; these include Alcaligenes eutrophus, A. denitrificans, A. faecalis, Paracoccus denitrificans and a no. of Pseudomonas species.

AN 1995:368281 CAPLUS
DN 122:284632
TI The FNR family of transcriptional regulators
AU Spiro, Stephen
CS School of Biological Sciences, University of East Anglia, Norwich, NR 7TJ, UK
SO Antonie van Leeuwenhoek (1994), 66(1-3), 23-36
CODEN: ALJMAO; ISSN: 0003-6072
PB Kluwer
DT Journal; ***General Review***
LA English

L7 ANSWER 19 OF 27 CAPLUS COPYRIGHT 2002 ACS

AB A review with 113 refs. Dissimilatory iron and/or manganese redn. is known to occur in several organisms, including anaerobic sulfur-reducing organisms such as Geobacter metallireducens or Desulfuromonas acetoxidans, and facultative aerobes such as Shewanella putrefaciens. These ***bacteria*** couple both carbon oxidn. and growth to the redn. of these metals, and inhibitor and competition expts. suggest that Mn(IV) and Fe(III) are efficient electron acceptors similar to nitrate in redox abilities and capable of out-competing electron acceptors of lower potential, such as sulfate (sulfate redn.) or CO2 (methanogenesis). Field studies of iron and/or manganese redn. suggest that organisms with such metabolic abilities play important roles in coupling the oxidn. of org. carbon to metal redn. under anaerobic conditions. Because both iron and manganese oxides are solids or colloids, they tend to settle downward in aquatic environments, providing a phys. mechanism for the movement of oxidizing potential into anoxic zones. The resulting biogeochem. metal cycles have a strong impact on many other elements including carbon, sulfur, phosphorus, and trace metals.

AN 1994:676254 CAPLUS
DN 121:276254
TI Iron and manganese in ***anaerobic*** ***respiration*** : environmental significance, physiology, and regulation
AU Nealson, Kenneth H.; Saffarini, Daad
CS Univ. Wisconsin-Milwaukee, Milwaukee, WI, 53204, USA
SO Annual Review of Microbiology (1994), 48, 311-43
CODEN: ARMIAZ; ISSN: 0066-4227
PB Annual Reviews
DT Journal; ***General Review***
LA English

L7 ANSWER 20 OF 27 CAPLUS COPYRIGHT 2002 ACS

AB A review with 192 refs. New obligately anaerobic ***bacteria*** are being discovered at an accelerating rate, and it is becoming very evident that the diversity of anoxic biotransformations has been greatly underestimated. Furthermore, among contemporary anaerobes there are many that thrive in extreme environments including, for example, an impressive array of both archaebacterial and eubacterial hyperthermophiles. Free energy for growth and reprodn. may be conserved not only via fermns. but also by anoxygenic photophosphorylation and other modes of creating transmembrane proton potential. Thus, forms of ***anaerobic*** ***respiration*** in which various inorg. oxidants (or indeed carbon dioxide) serve as terminal electron acceptors have greatly extended the natural habitats in which such organisms may predominate. Anaerobic ***bacteria*** are, however, often found in nature as members of close microbial communities (consortia) that, although sustained by syntrophic and other relations between component species, are liable to alter their compn. and character in response to environmental changes, e.g., availability of terminal oxidants. It follows that the biotechnol. exploitation of obligately anaerobic ***bacteria*** must be informed by knowledge both of their biochem. capacities and of their normal environmental roles. It is against this background that illustrative examples of the activities of anaerobic ***bacteria*** are considered under three heads: (1) biodegrdn./bioremediation, with special ref. to the anaerobic breakdown of arom. and/or halogenated org. substances; (2) biosynthesis/bioprodn., encompassing normal and modified fermns.; and (3) biotransformations, accomplished by whole or semipermeabilized organisms or by enzymes derived therefrom, with particular interest attaching to the prodn. of chiral compds. by a no. of procedures, including electromicrobial redn.

AN 1994:577756 CAPLUS

DN 121:177756
TI Obligately anaerobic ***bacteria*** in biotechnology
AU Morris, J. Gareth
CS Inst. Biological Sciences, Univ. Wales, Aberystwyth/Penglais/Aberystwyth, SY23 3DA, UK
SO Applied Biochemistry and Biotechnology (1994), 48(2), 75-106
CODEN: ABIBDL; ISSN: 0273-2289
DT Journal; ***General Review***
LA English

L7 ANSWER 21 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 224 refs. Genetically constructed N_2-fixing strains from authentic Pseudomonas species have demonstrated that at least some members of the genus possess mechanisms to accommodate and express nif (N_2 fixation) genes from a well-studied diazotroph, Klebsiella pneumoniae. Potential N_2-fixing pseudomonads are conceivably less limited by carbon and energy sources available in the environment compared to other N_2-fixing organisms. Pseudomonas species dominate in the rhizosphere of some plants from which isolates have been shown to be diazotrophic. Several strains are also chemolithotrophs, capable of using H_2 as energy and electron source and CO_2 as carbon source. Besides assays for N_2-fixing activity, DNA hybridization to the well conserved molybdo-nitrogenase structural gene probe is an indicator of diazotrophy. Although the genetics of N_2 fixation in pseudomonads have hardly been studied, some nif genes have been shown to be plasmid-borne. Pseudomonas species are also predominant soil denitrifiers, reducing nitrate and nitrite to gaseous forms of nitrogen during ***anaerobic*** ***respiration*** . Hence, they play an important role in the global biol. nitrogen cycle. Several diazotrophic species including a few pseudomonads can also denitrify. The potential contribution by N_2-fixing pseudomonads to the sinks and sources of soil nitrogen is considered small in the short term but essentially remains unclear in the absence of exptl. data. Reliable rapid methods for their specific enumeration are indispensable for assessing their population dynamics and ascertaining their ecol. significance.
AN 1994:158239 CAPLUS
DN 120:158239
TI N_2-fixing pseudomonads and related soil ***bacteria***
AU Chan, Yiu Kwok; Barraquio, Wilfredo L.; Knowles, Roger
CS Plant Res. Cent., Agric. Canada, Ottawa, ON, K1A 0C6, Can.
SO FEMS Microbiology Reviews (1994), 13(1), 95-117
CODEN: FMREE4; ISSN: 0168-6445
DT Journal; ***General Review***
LA English

L7 ANSWER 22 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 40 refs. on the aerobic and anaerobic pathways for MnO_2 redn. by ***bacteria*** .
AN 1988:52461 CAPLUS
DN 108:52461
TI Manganese oxide reduction as a form of ***anaerobic*** ***respiration***
AU Ehrlich, Henry L.
CS Dep. Biol., Rensselaer Polytech. Inst., Troy, NY, 12180-3590, USA
SO Geomicrobiol. J. (1987), 5(3-4), 423-31
CODEN: GEJODG; ISSN: 0149-0451
DT Journal; ***General Review***
LA English

L7 ANSWER 23 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 136 refs. on pathways of anaerobic electron transport in the Rhodospirillaceae. Emphasis is given to the possibility that, apart from a role in energy conservation, ***anaerobic*** ***respiration*** in the photosynthetic ***bacteria*** may have a special function in maintaining redox balance during photosynthetic metab. Thus, electron acceptors such as trimethylamine-N-oxide, DMSO, NO_3^-, and NO may serve as auxiliary oxidants: (a) to maintain an optimal redox poise of the photosynthetic electron transport chain; (b) to provide a sink for electrons during phototrophic growth on highly reduced carbon substrates.
AN 1987:493450 CAPLUS
DN 107:93450
TI ***Anaerobic*** ***respiration*** in the Rhodospirillaceae: characterization of pathways and evaluation of roles in redox balancing during photosynthesis
AU Ferguson, Stuart J.; Jackson, J. Barry; McEwan, Alastair G.
CS Dep. Biochem., Univ. Oxford, Oxford, OX1 3QU, UK
SO FEMS Microbiol. Rev. (1987), 46(2), 117-43

CODEN: FMREE4
DT Journal; ***General Rev[illegible]***
LA English

L7 ANSWER 24 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 34 refs. Many anaerobic ***bacteria*** gain ATP not only from substrate level phosphorylation, but also by electron transport coupled phosphorylation. These reactions resemble the oxidative phosphorylation of aerobic ***bacteria*** and are, therefore, termed ***anaerobic*** ***respiration*** . In contrast to aerobic respiration where oxygen serves as the terminal electron acceptor, redox couples with extremely electroneg. potentials can be used as acceptors in ***anaerobic*** ***respiration*** . As a consequence, the ATP yields may be very small, and part of the electron transport reactions may be reversed at the energetic expense of others.
AN 1987:172493 CAPLUS
DN 106:172493
TI Direct and reversed electron transport in anaerobic ***bacteria***
AU Kroeger, A.; Schroeder, I.; Paulsen, J.
CS Inst. Mikrobiol., Johann Wolfgang Goethe-Univ., Frankfurt, Fed. Rep. Ger.
SO Prog. Biotechnol. (1986), 2(Biol. Anaerobic Bact.), 93-104
CODEN: PBITE3
DT Journal; ***General Review***
LA English

L7 ANSWER 25 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review, with 49 refs., on anaerobic ***bacteria*** , discussing fermns., energized cell membrane, ***anaerobic*** ***respiration*** , anoxygenic photophosphorylation, ATP, growth yield, and utility of growth yield measurements.
AN 1986:549370 CAPLUS
DN 105:149370
TI Anaerobiosis and energy-yielding metabolism
AU Morris, J. G.
CS Dep. Bot. Microbiol., Univ. Coll. Wales, Aberystwyth/Dyfed, SY23 3DA, UK
SO Soc. Appl. Bacteriol. Symp. Ser. (1986), 13(Anaerobic Bact. Habitats Other Than Man), 1-21
CODEN: SAPBB7; ISSN: 0300-9610
DT Journal; ***General Review***
LA English

L7 ANSWER 26 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 99 refs. Inorg. S compds. are used by microorganisms (***bacteria*** , fungi, algae) and plants for assimilation, i.e. biosynthesis of S-contg. cell constituents. Quant., within the biogeochem. cycle of S, the utilization of inorg. S compds. in bacterial energy metab., i.e. dissimilatory S utilization, is of far higher importance. Reduced S compds. serve as electron donors for photosynthesis and respiration, whereas inorg. S compds. of oxidn. levels above sulfide serve as electron donors in ***anaerobic*** ***respiration*** as well as in fermn. In still other ***bacteria*** , reduced S compds. act as protective agents against H_2O_2.
AN 1985:519421 CAPLUS
DN 103:119421
TI Microbial metabolism of inorganic sulfur compounds
AU Trueper, Hans G.
CS Inst. Mikrobiol., Rheinischen Friedrich Wilhelms-Univ., Bonn, D-5300, Fed. Rep. Ger.
SO Phosphorus Sulfur (1985), 24(1-2), 545-78
CODEN: PREEDF; ISSN: 0308-664X
DT Journal; ***General Review***
LA English

L7 ANSWER 27 OF 27 CAPLUS COPYRIGHT 2002 ACS
AB A review with 31 refs. of sulfate as the terminal electron acceptor in ***anaerobic*** ***respiration*** by Desulfovibrio and Desulfotomaculum.
AN 1981:437168 CAPLUS
DN 95:37168
TI Dissimilatory sulfate reduction, mechanistic aspects
AU Akagi, J. M.
CS Dep. Microbiol., Univ. Kansas, Lawrence, KS, 66045, USA
SO Biol. Inorg. Nitrogen Sulfur, [Conf.] (1981), Meeting Date 1980, 178-87. Editor(s): Bothe, Hermann; Trebst, Achim. Publisher: Springer, Berlin, Fed. Rep. Ger.
CODEN: 45SAA9
DT Conference; ***General Review***

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LA   English

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     FILE 'CAPLUS' ENTERED AT 09:10:24 ON 09 OCT 2002
L1      1579360 S REVIEW/DT
L2          609 S ANAEROBIC RESPIRATION
L3           34 S OXIDANT SOURCE
L4           61 S L1 AND L2
L5            0 S L3 AND L4
L6       238628 S BACTERIA
L7           27 S L4 AND L6

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